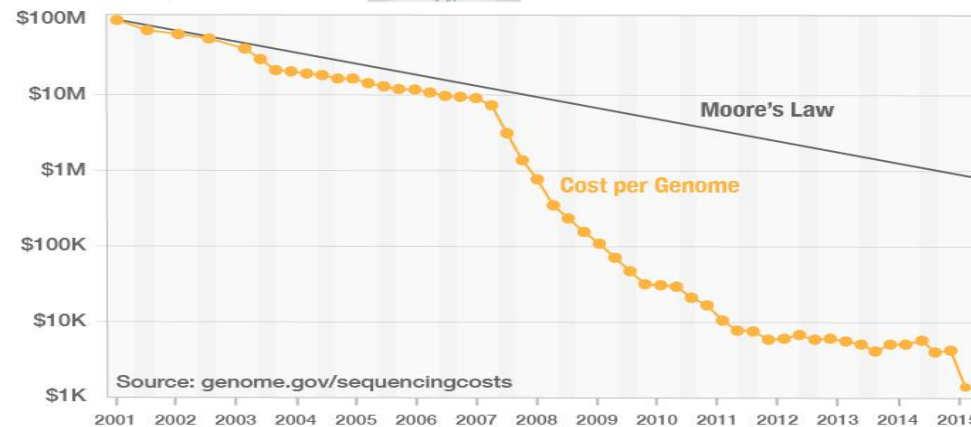
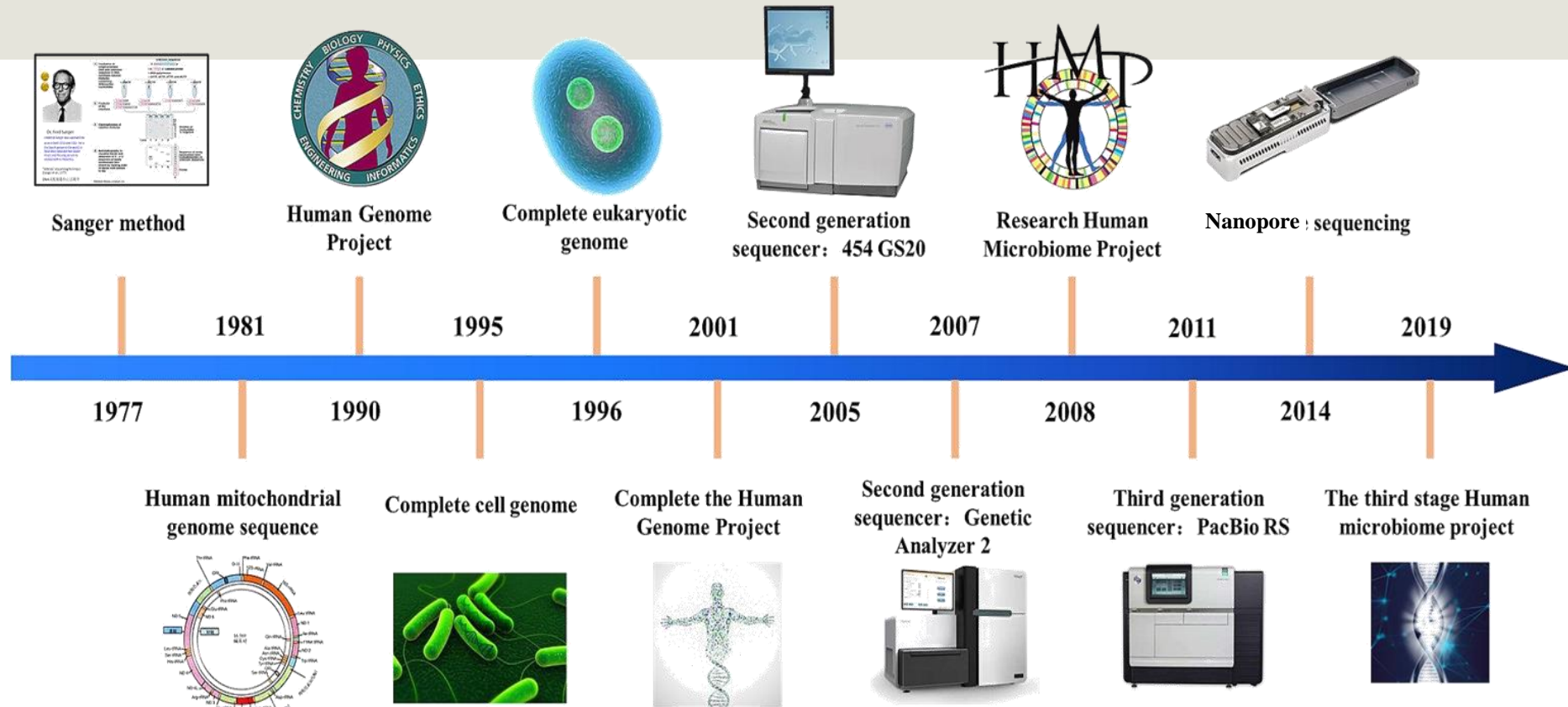


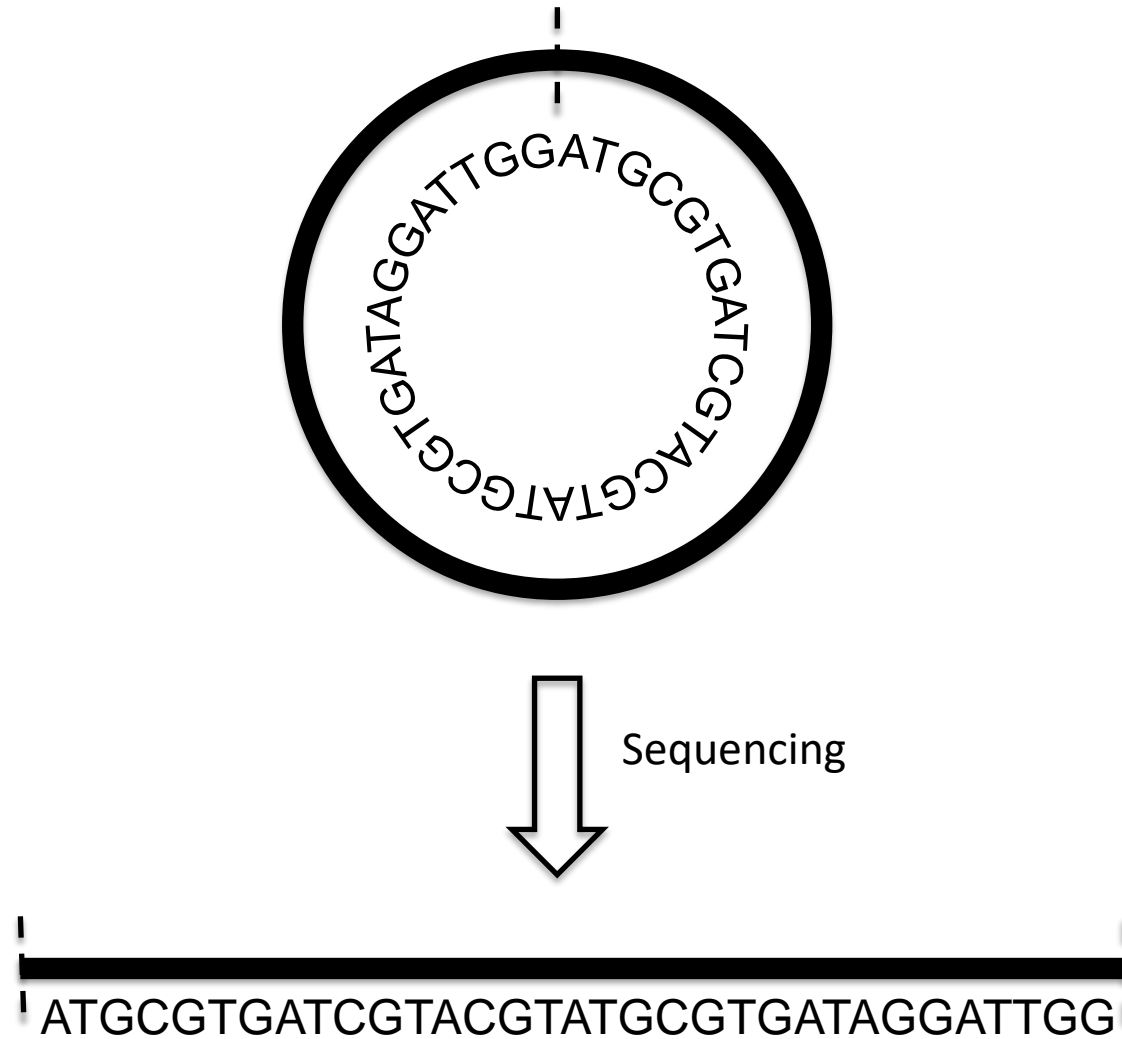
# Rio Grande RS 2023

Figure 1: Overview of the experimental workflow. (a) Schematic of the experimental workflow showing the process from cell culture to sequencing. (b) Word cloud of sequencing-related terms. (c) Schematic of the sequencing process showing the flow of DNA and the resulting sequencing data.

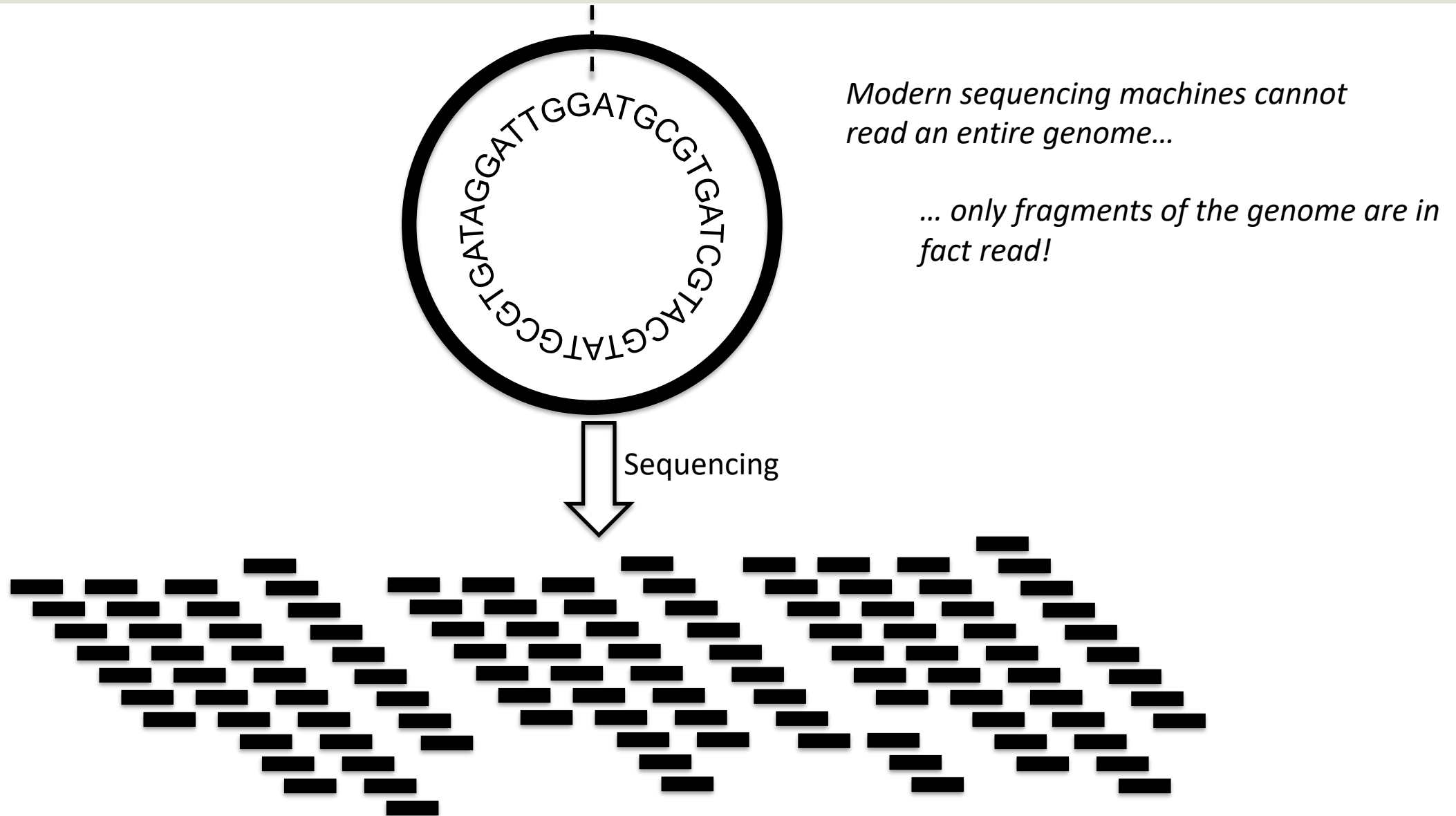
# Sequencing through time...







## Genome Sequencing: Ideal situation...



## Genome Sequencing: the hard reality...



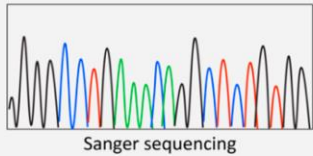
## NGS Platforms: An overview ...

				
<b>Read Length (bp)</b>	<b>50-300</b>	<b>200-400</b>	<b>10000-40000</b>	<b>1Mbp</b>
<b>Output (Gb)</b>	<b>6000</b>	<b>0,05-1</b>	<b>0,5-1</b>	<b>5-40</b>
<b>Cost / Million bp (USD)</b>	<b>0,05-0,15</b>	<b>1</b>	<b>0,13-0,60</b>	<b>variable</b>
<b>Accuracy</b>	<b>99.9%</b>	<b>99.6%</b>	<b>87%</b>	<b>92-97%</b>
<b>Time per run</b>	<b>1-11d</b>	<b>2h</b>	<b>30min-20h</b>	<b>1min-48h</b>

**Sanger Cost per MB: 2400USD**

# Next Generation Sequencing

## A First generation sequencing



Targeted sequencing

### Advantages

- + Accuracy
- + Costs (< 20 amplicons)
- + Turnaround time

### Disadvantages

- Capacity
- Costs (>20 amplicons)
- Throughput

## B Next generation sequencing



Illumina whole  
exome sequencing



Illumina whole  
genome sequencing

Short read sequencing

### Advantages

- + Applicability
- + Costs
- + Throughput

### Disadvantages

- Coverage and mapping
- Data interpretation
- Structural variant detection

## C Third generation sequencing



SMRT sequencing



Nanopore sequencing

Long read sequencing

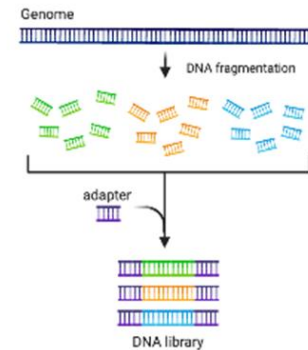
### Advantages

- + Coverage and mapping
- + De novo assembly
- + Structural variant detection

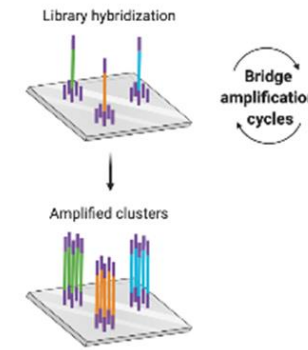
### Disadvantages

- Accuracy
- Costs
- Library preparation

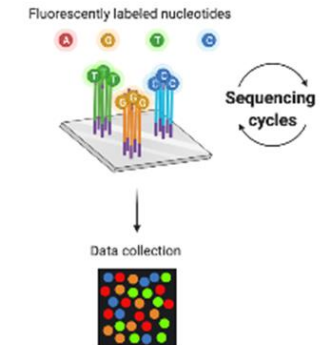
## 1 Library preparation



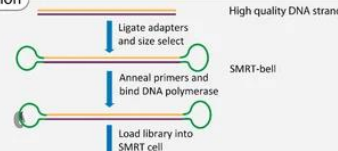
## 2 DNA library bridge amplification



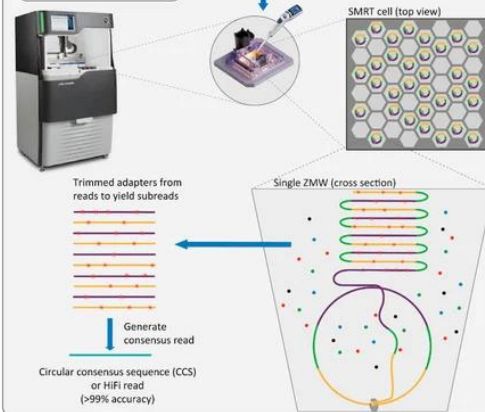
## 3 DNA library sequencing



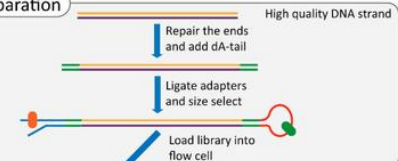
## A Library preparation



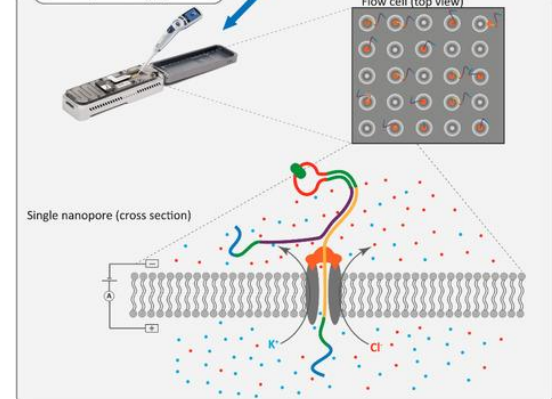
## B Sequencing process



## A Library preparation



## B Sequencing process





# Illumina: Sequencing-by-synthesis

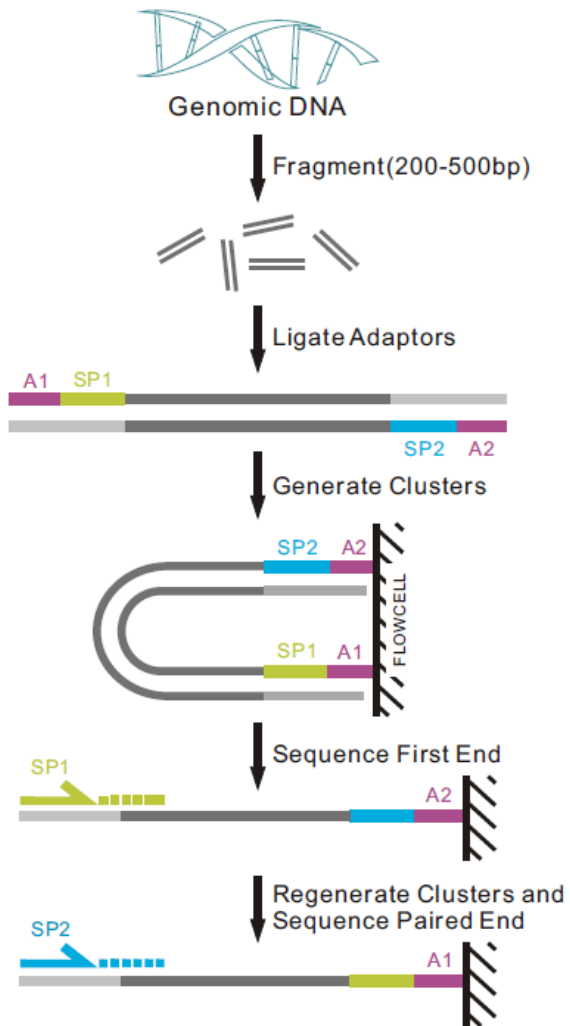
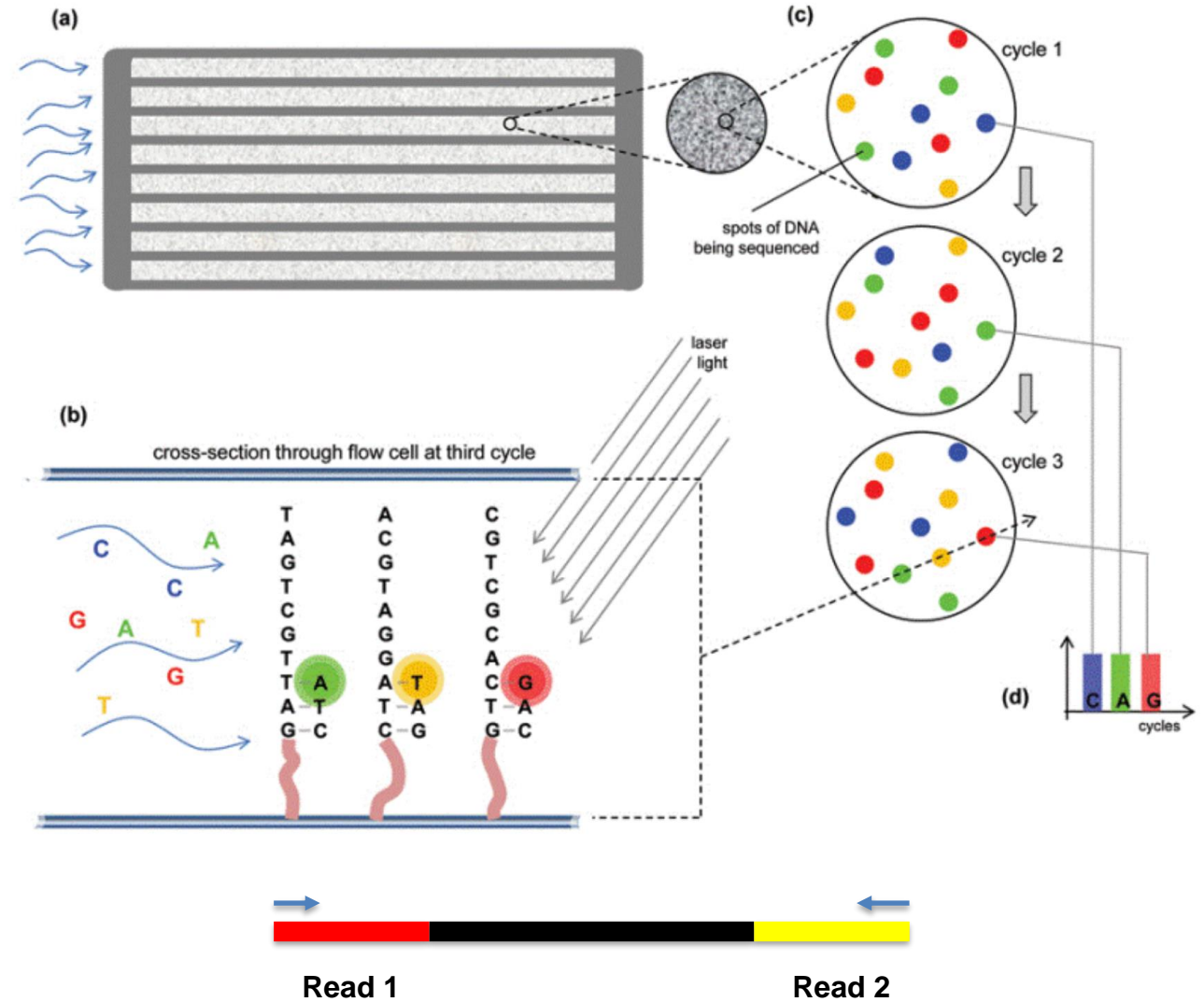
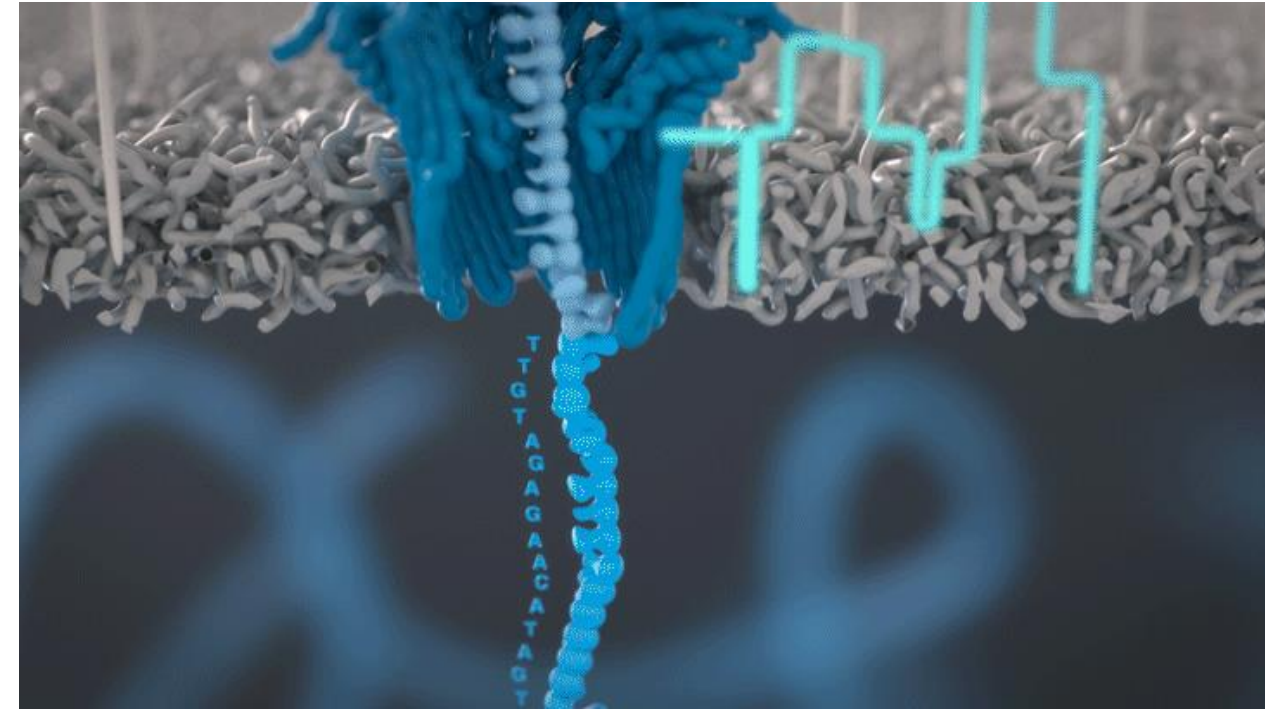
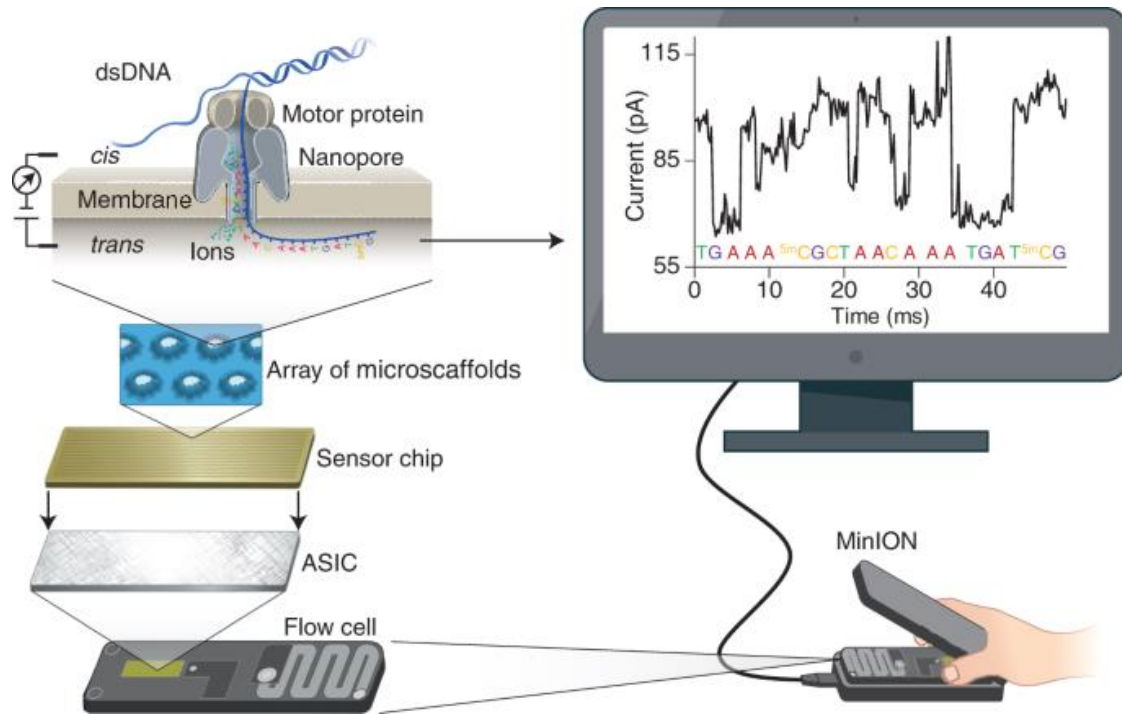


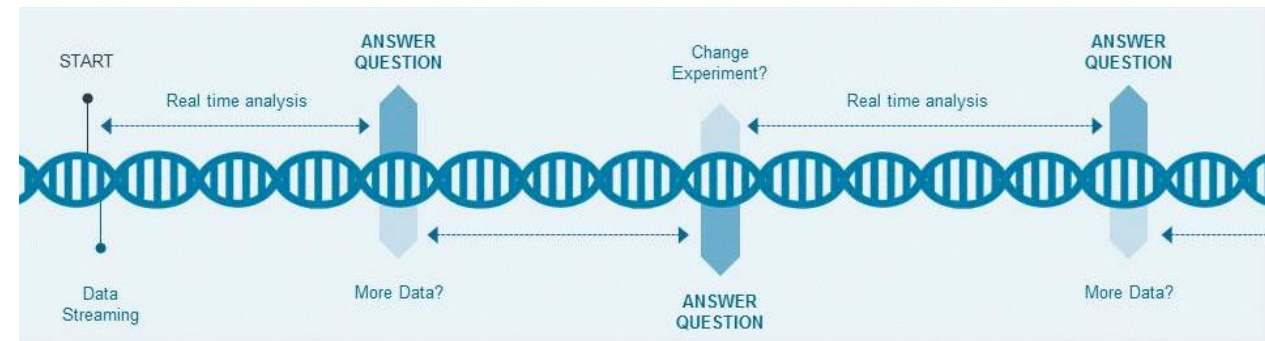
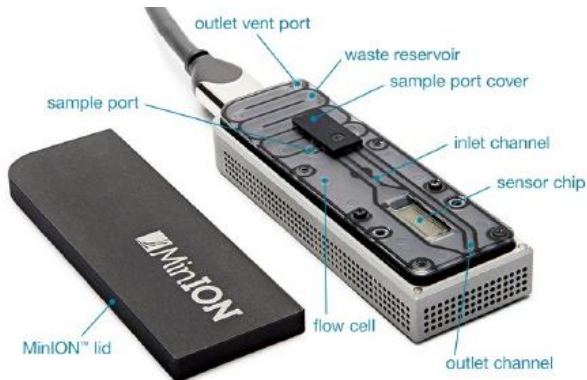
Figure 1-2-1 Pipeline of paired-end sequencing (www.illumina.com)



# Oxford Nanopore: nanopore sequencing with real-time analysis

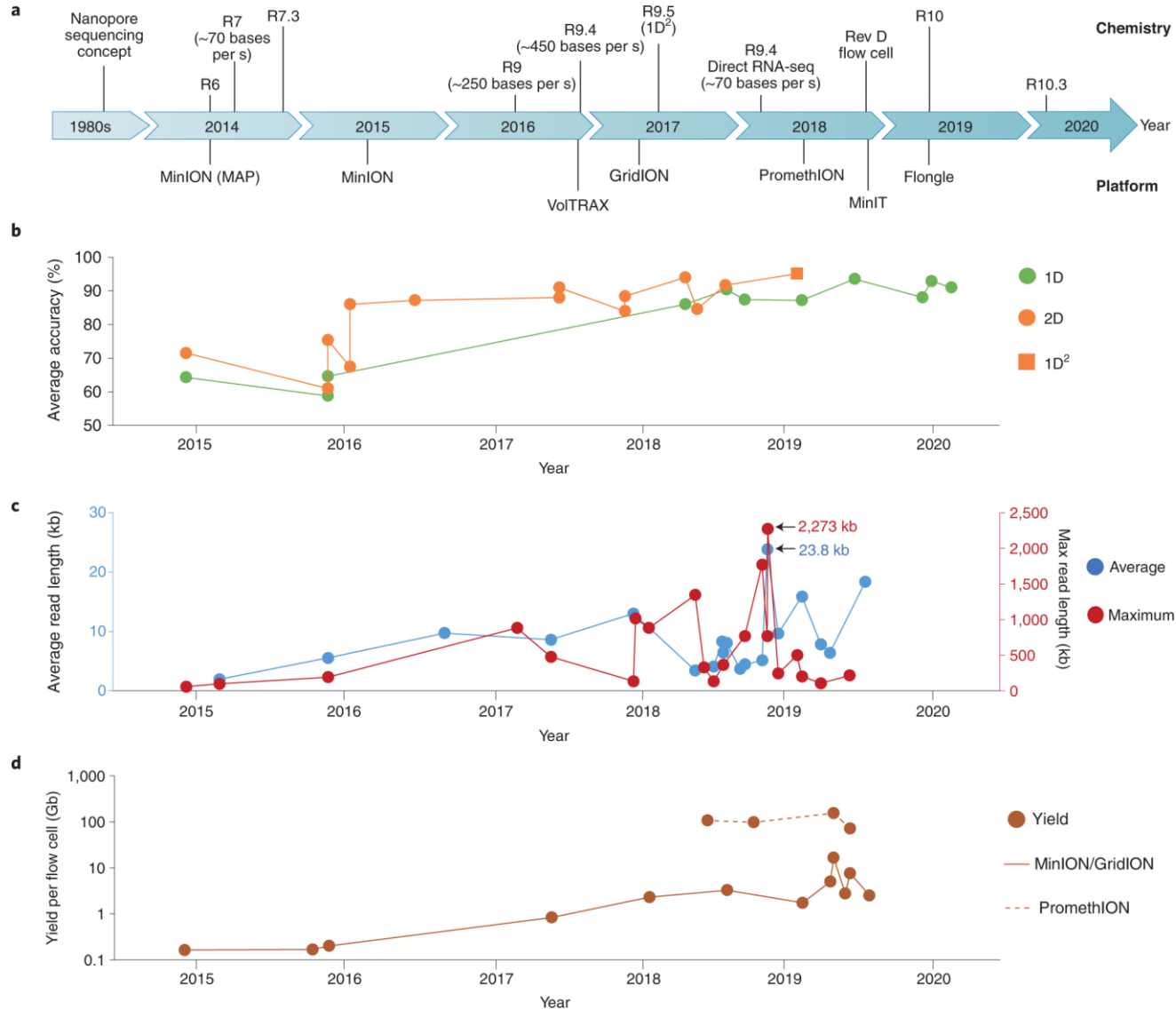


*Wang et al 2021*

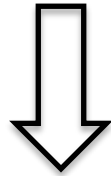
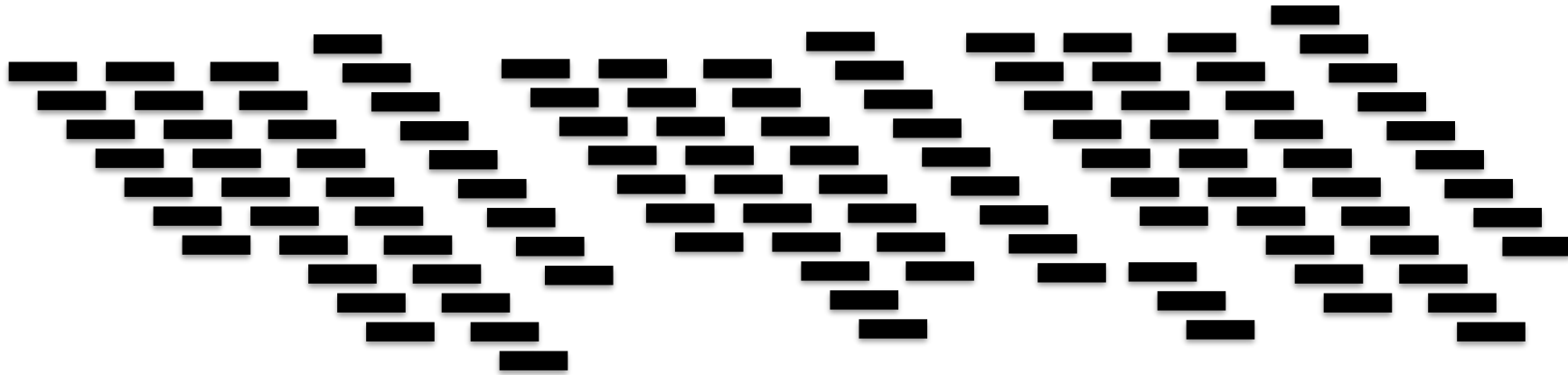




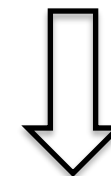
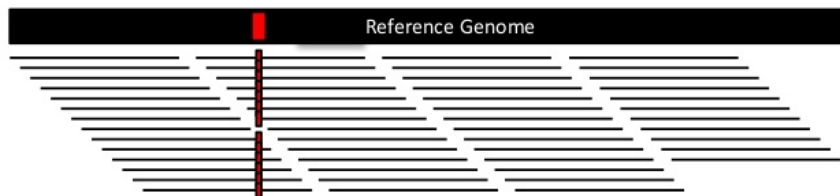
# Oxford Nanopore: nanopore sequencing with real-time analysis



## Two main approaches for handling reads...



### Mapping or Reference Assembly

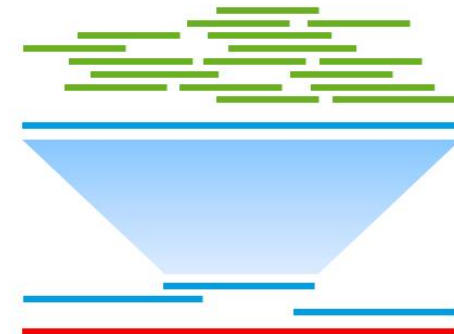


### *De novo* Assembly

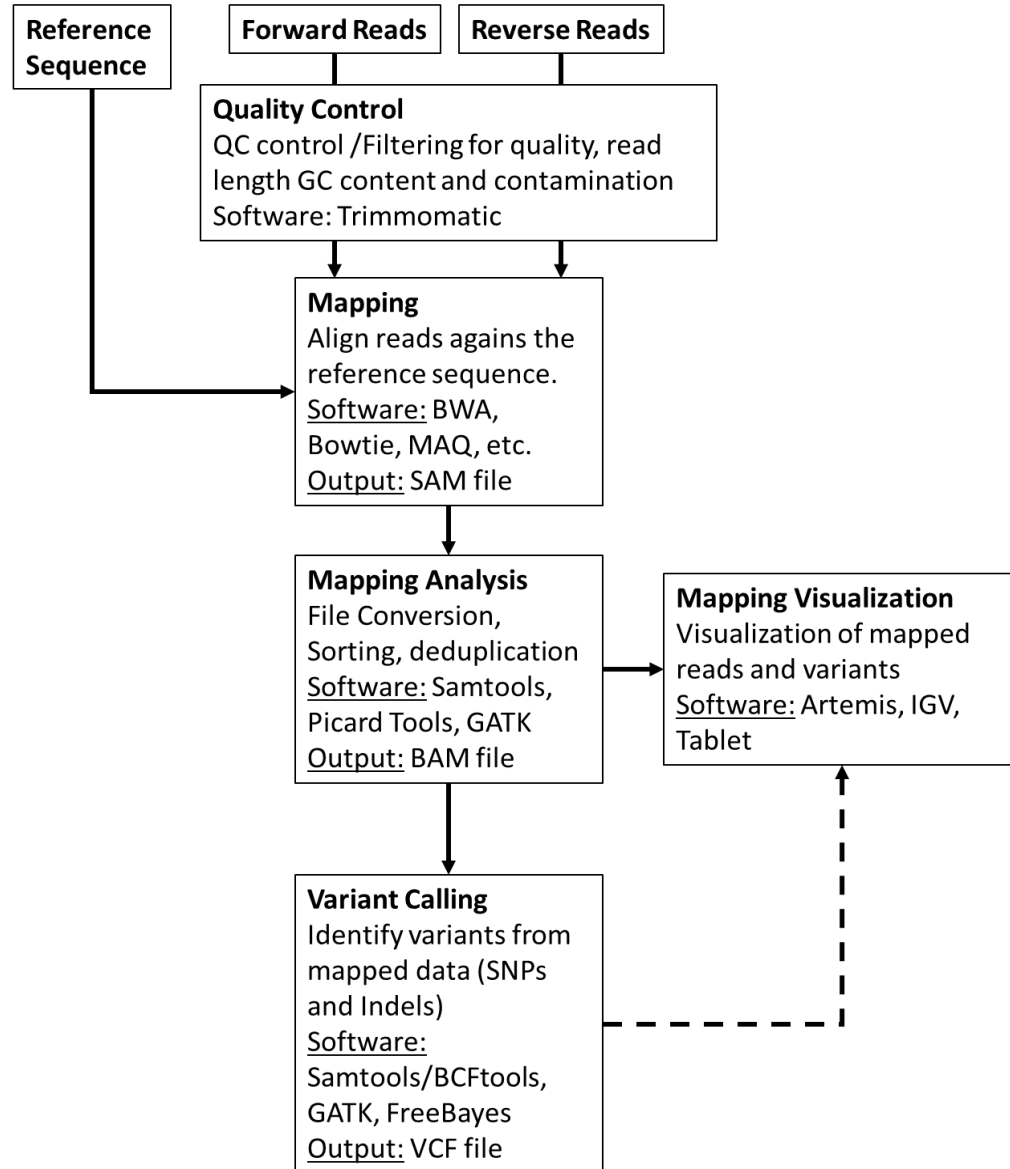
Short / Long reads

Contig assembly

Scaffold assembly  
Finished genome



# Workflow



## Four main analytical stages:

- *Quality-control* – filter out reads/bases associated with poor basecall quality;
- *Mapping* – map reads to a reference genome, obtain sample coverage at each position and read coordinates;
- *Variant Calling* – identify variants existing between sequenced and reference genome, either SNPs or INDELs;
- *Functional Annotation* – determine the functional impact of each variant, e.g., which gene is affected? Is the mutation synonymous or non-synonymous? impact at the peptide primary structure?

## What storage format for Sequencing Reads: FASTA vs FASTQ

# FASTA

The diagram illustrates the structure of a FASTA file. It features a header line starting with a greater-than sign (>) followed by a file path and a description. Below the header are multiple lines of sequence data. Labels with colored lines pointing to the corresponding parts of the FASTA file are as follows:

- Label** (yellow line): Points to the file path part of the header.
- Title Line** (blue line): Points to the description part of the header.
- Comment** (pink line): Points to the description part of the header.
- Data Lines** (cyan line): Points to the sequence data lines.

**FASTA File Content:**

```
>fig|282458.1.peg.1 Chromosomal replication initiator protein dnaA
MSEKEIWEKVLEIAQEKLSAVSYSTFLKDTELYTIKDGEAIVLSSIPFNANWLNQYAEI
IQAILFDVVGVEVKPHFITTEELANYSNNETATPKPEATKPSTETTEDNHVLGREQFNAHN
TFDTFVIGPNRPFHAASLAVAEAPAKAYNPLFIYGGVGLGKTHLMAIGHHVLDDNNPDA
KVIYTSSEKFTNEFIKSIRDNEGEAFRERYRNIDVLLIDDIQFIQNKVQTQEEFFYTFNE
LHQNKKQIVISSDRPPKEIAQLEDRLRSRFEWGLIVDITPPDYETRMALIQKKIEEEKLD
IPPEALNYIANQIQSNIRELEGALTRLLAYSQLLGKPITTELTAELKDI IQAPKSKKIT
IQDIQKIVGQYYNVRIEDFSAKGRKTSIAYPRQIAMYLSRELTD FSLPKIGEEFGGRDHT
TVIHAHEKISKDLKEDPIFKQEVENLEKEIRNV
```

## FASTQ

[illegible]

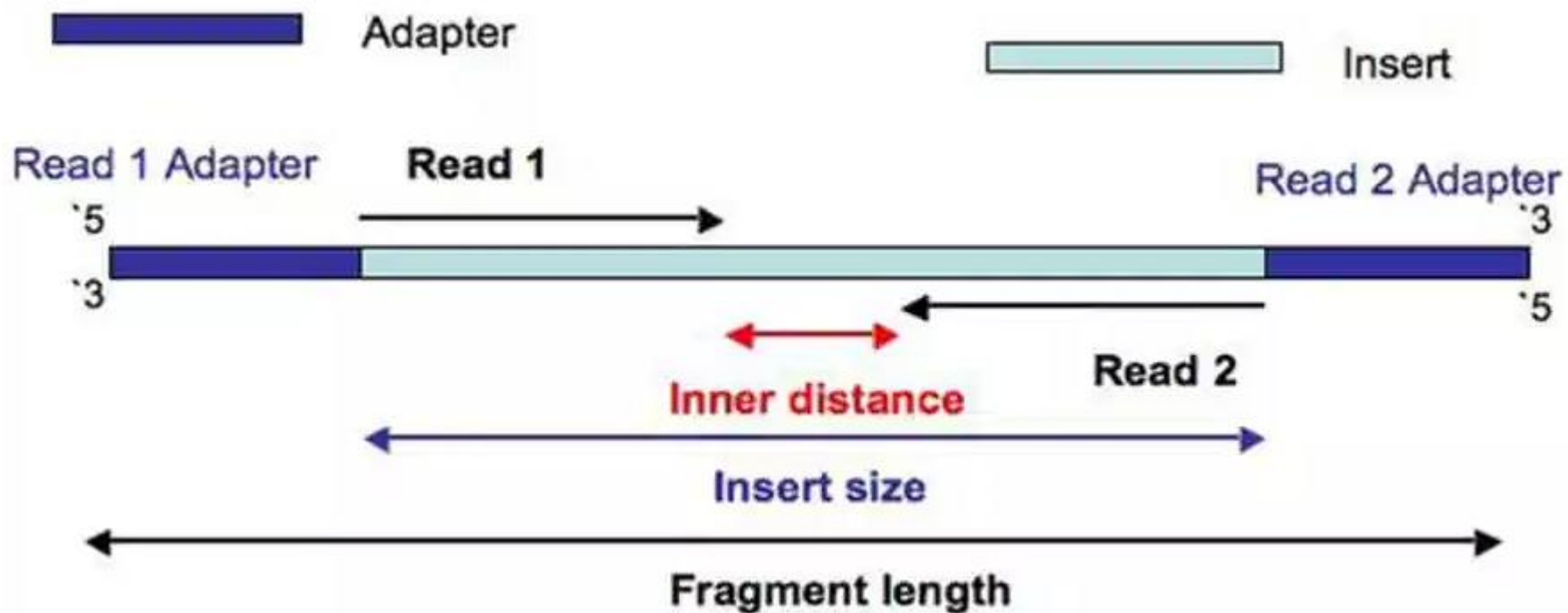
Sequence quality: ◀

ASCII encoded Phred-33 quality score for each nucleotide of the sequence read above. Example: the 3rd nucleotide in the bottom read has a quality (Phred33 Q) of 28. Check the table below. What about the 5th nucleotide of the same read?

ASCII_BASE=33 Illumina, Ion Torrent, PacBio and Sanger											
Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII
0	1.00000	33 !	11	0.07943	44 ,	22	0.00631	55 7	33	0.00050	66 B
1	0.79433	34 "	12	0.06310	45 -	23	0.00501	56 8	34	0.00040	67 C
2	0.63096	35 #	13	0.05012	46 .	24	0.00398	57 9	35	0.00032	68 D
3	0.50119	36 \$	14	0.03981	47 /	25	0.00316	58 :	36	0.00025	69 E
4	0.39811	37 %	15	0.03162	48 0	26	0.00251	59 ;	37	0.00020	70 F
5	0.31623	38 &	16	0.02512	49 1	27	0.00200	60 <	38	0.00016	71 G
6	0.25119	39 '	17	0.01995	50 2	28	0.00158	61 =	39	0.00013	72 H
7	0.19953	40 (	18	0.01585	51 3	29	0.00126	62 >	40	0.00010	73 I
8	0.15849	41 )	19	0.01259	52 4	30	0.00100	63 ?	41	0.00008	74 J
9	0.12589	42 *	20	0.01000	53 5	31	0.00079	64 @	42	0.00006	75 K
10	0.10000	43 +	21	0.00794	54 6	32	0.00063	65 A			

# What storage format for Sequencing Reads: FASTA vs FASTQ

*Why do I get two FastQ files?*



<https://thesequencingcenter.com/knowledge-base/what-are-paired-end-reads/>

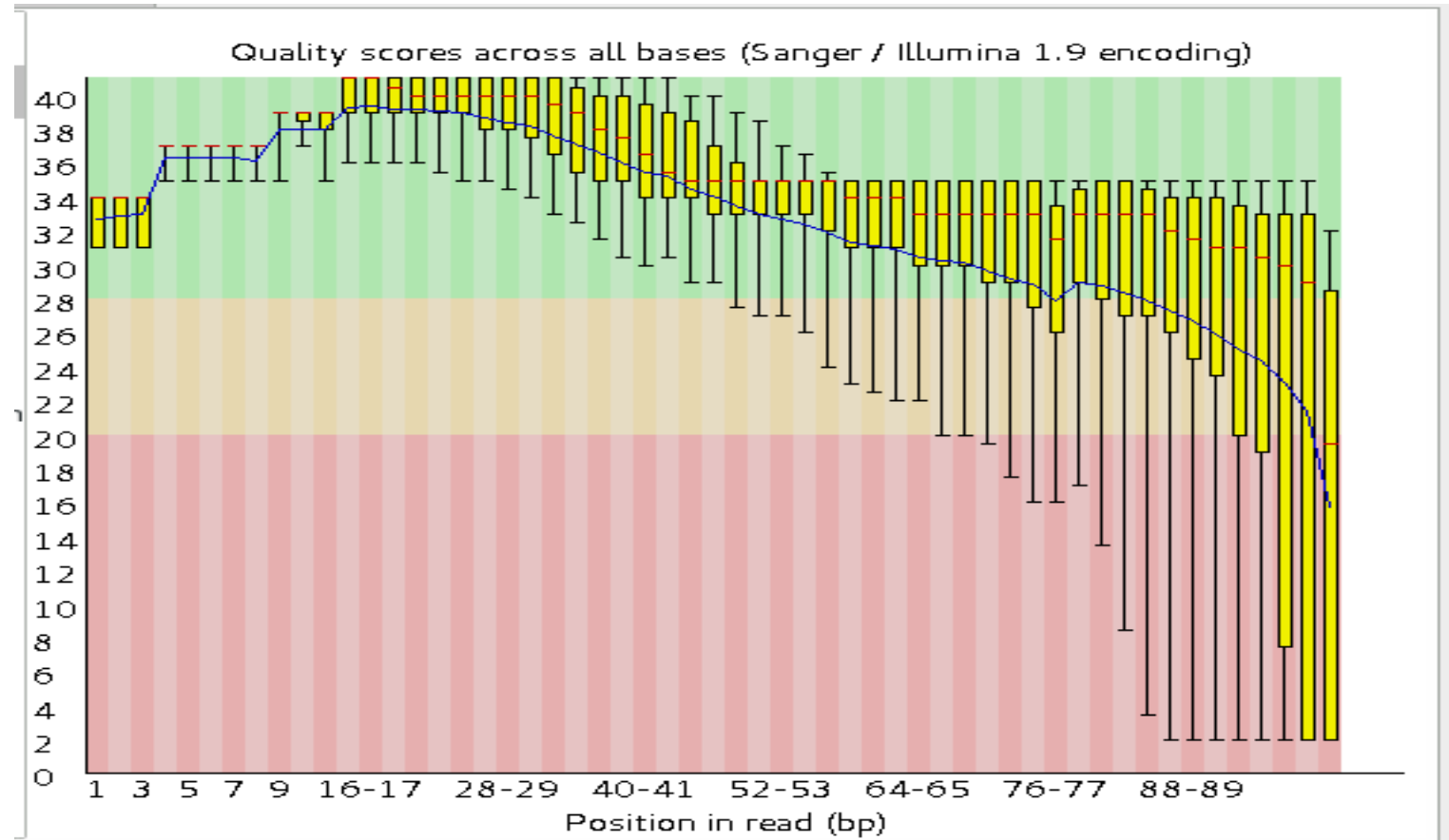


# Quality Control: Assessment

## Objective:

- Assess overall sequencing quality and assess if sequencing metrics are within expected ranges;
- Remove base calls associated with low quality by removing or trimming sequencing reads;
- Taxonomical read QC – *did you sequence what you thought you did?*

**Main/Most frequent problem:** base quality deterioration along the read length



# Quality Control: Assessment

## How to assess sequencing metrics?

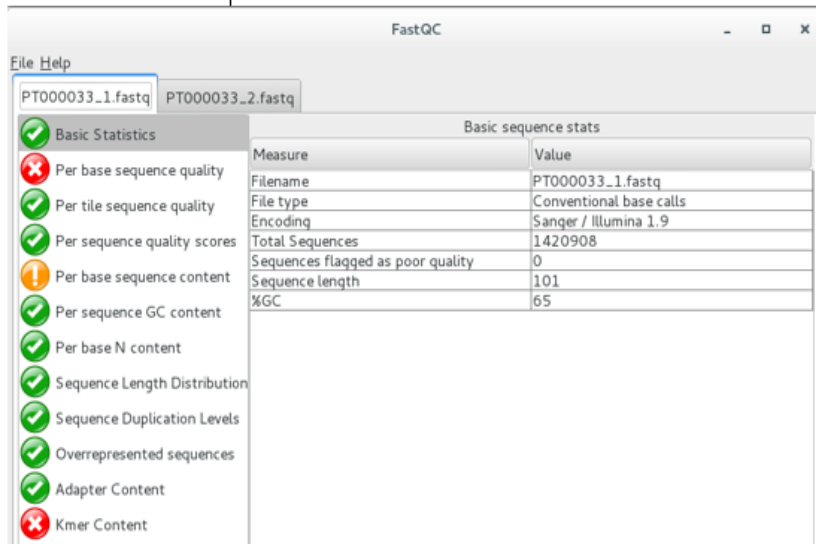
**Software:** FastQC, AfterQC, fastqp, HTSeq, etc.

FastQC – Java tool with both GUI and command-line as options.

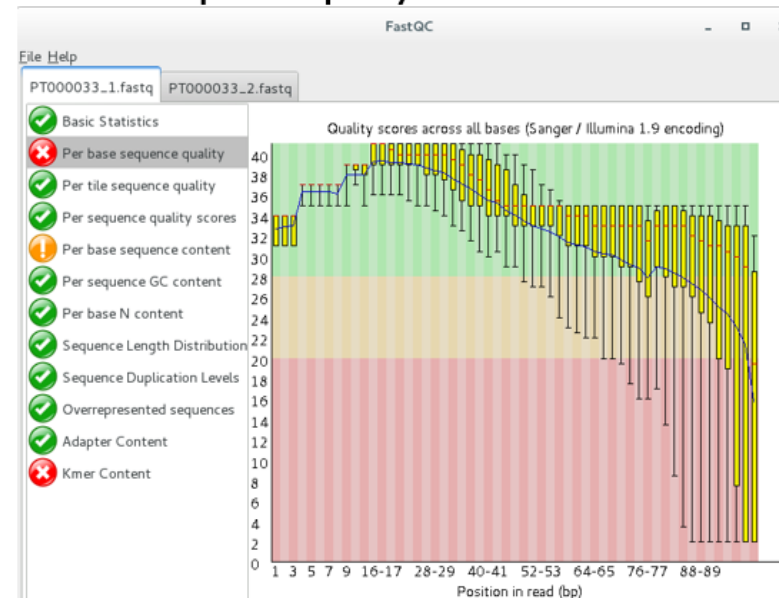
**Input:** FastQ files  
(or SAM/BAM files)

**Output:** sequencing  
metrics and plots

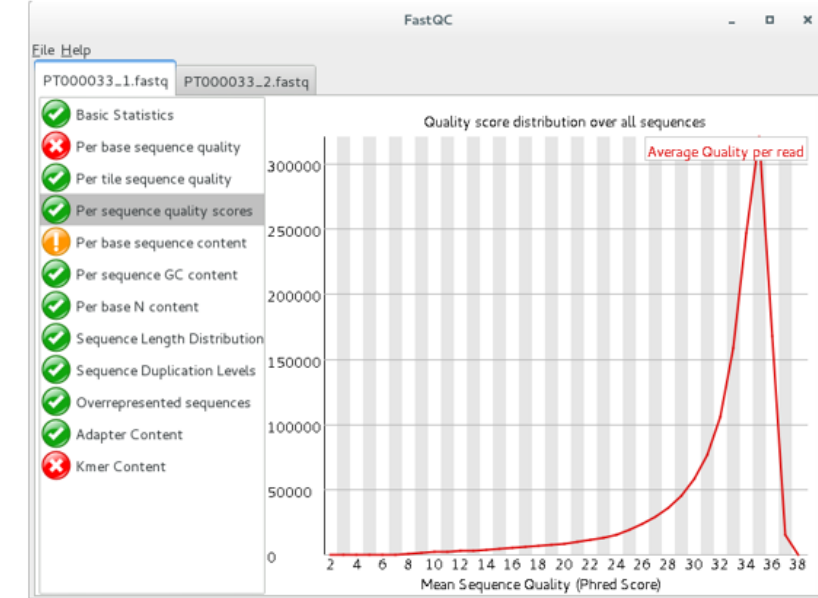
### Basic Statistics



### Per base sequence quality



### Per sequence quality score



# Quality Control: Assessment

## How to assess sequencing metrics?

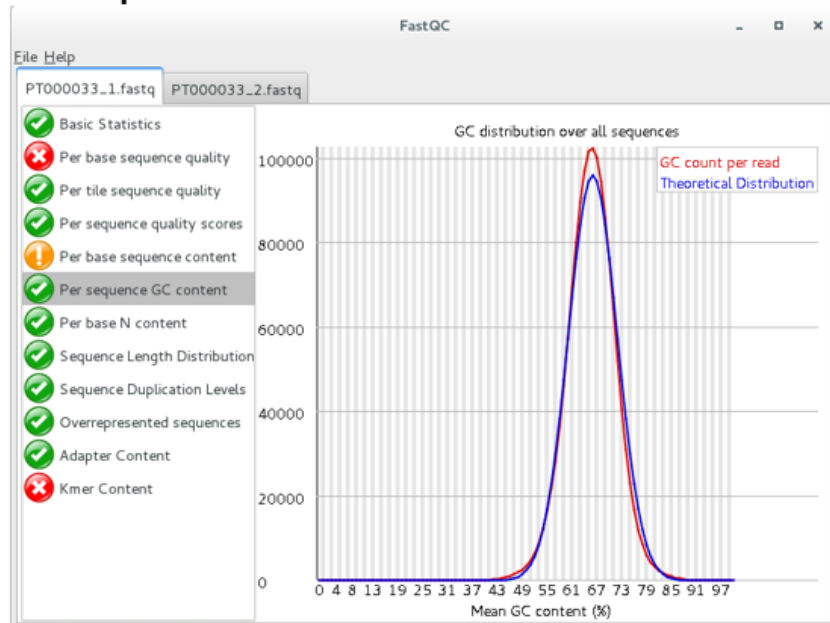
**Software:** FastQC, AfterQC, fastqp, HTSeq, etc.

FastQC – Java tool with both GUI and command-line as options.

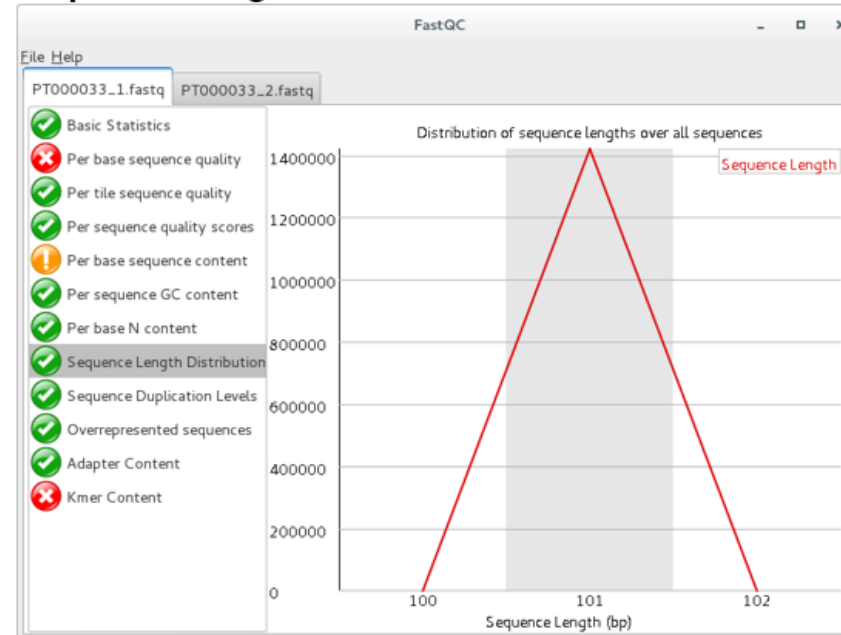
**Input:** FastQ files  
(or SAM/BAM files)

**Output:** sequencing  
metrics and plots

### Per Sequence GC content



### Sequence Length Distribution



# Quality Control: Correction

## How to correct, cut and filter out sequencing reads?

**Software:** Trimmomatic, FASTX, etc.

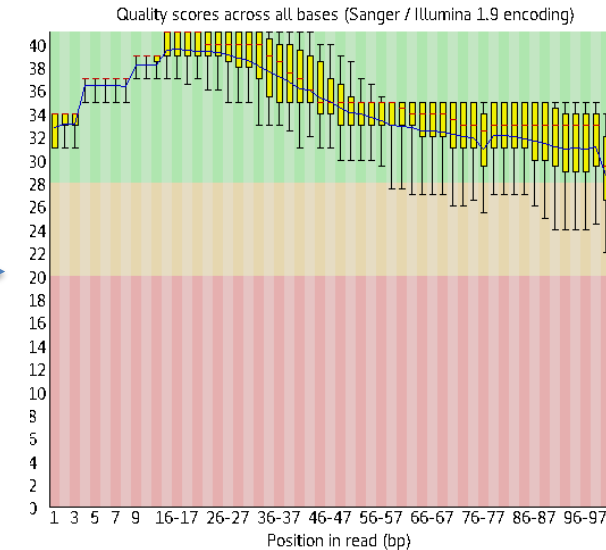
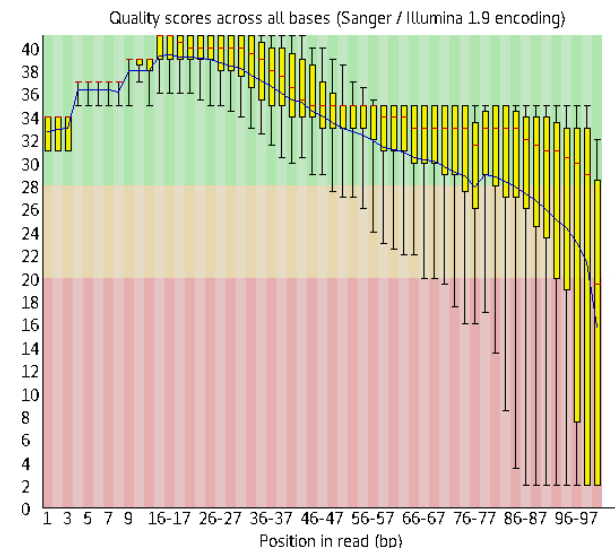
Trimmomatic – command-line Java tool capable of handling SE and PE reads.

**Input:** FastQ files.

**Output:** FastQ files with  
trimmed/cut and surviving reads.

**Trimmomatic can:**

- Remove adapters;
- Remove leading and trailing low quality bases;
- Cut reads upon scanning at user defined sliding Windows when below a specified threshold;
- Remove reads when these don't meet a specified minimum length.



# Quality Control: Taxonomical Read QC

*Did I sequence what I thought I did? or Why doesn't it map? or Why does the assembly look strange?*

**Software:** Kraken

Kraken – command-line tool that assigns reads to different taxonomical clades.

**Input:** FastQ files.

**Output:** Text Report.

0.89	28702	28702	U	0	unclassified	3.65	137472	137472	U	0	unclassified
99.11	3210397	42095	-	1	root	96.35	3631172	7288	-	1	root
97.81	3168297	1864	-	131567	cellular organisms	96.16	3623815	2151	-	131567	cellular organisms
97.76	3166433	16142	D	2	Bacteria	96.10	3621664	10917	D	2	Bacteria
97.25	3150142	4158	P	1224	Proteobacteria	95.81	3610594	13835	P	1224	Proteobacteria
97.12	3145930	19183	C	1236	Gammaproteobacteria	95.43	3596429	40211	C	1236	Gammaproteobacteria
94.74	3068819	83719	O	91347	Enterobacterales	92.48	3485213	108814	O	91347	Enterobacterales
92.16	2985015	1245831	F	543	Enterobacteriaceae	89.53	3374249	342184	F	543	Enterobacteriaceae
53.46	1731479	124411	G	561	Escherichia	79.20	2984764	1375209	G	570	Klebsiella
49.60	1606565	1603919	S	562	Escherichia coli	38.86	1464425	1415727	S	573	Klebsiella pneumoniae



# Mapping or Reference Assembly

**Objective:** Find the origin of a sequencing read providing a reference genome is known

**Reference genome:** Should be a high quality genome, ideally finished, the close as possible to the sequenced genome.

**Software:** Burrows-Wheeler Aligner (BWA), Bowtie2, HISAT2

**Input:** FastQ files.

**Output:** Mapped/Alignment File  
SAM/BAM file

Most mapping software implement the Burrows-Wheeler transformation algorithm which enables fast access to sequence data with an acceptable memory footprint.

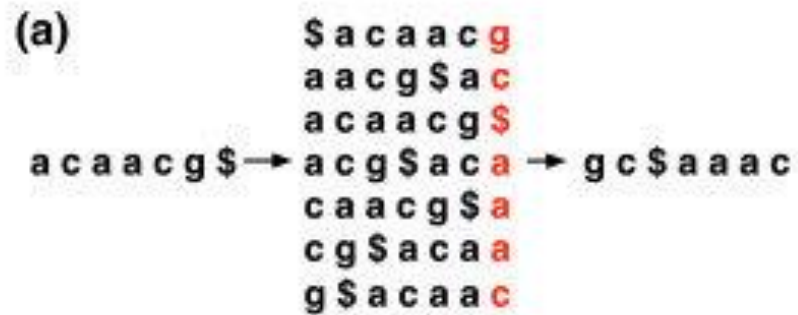
Ins. (bp)	Execution time				Memory usage				Accuracy				% Prop. paired reads			
	350		550		350		550		350		550		350		550	
RL (bp)	100	150	100	150	100	150	100	150	100	150	100	150	100	150	100	150
BWA	+	+	+	+	+	+	+	+	+++	+++	+++	+++	+++	+++	+++	+++
Bowtie2	++	++	++	++	+++	+++	++	++	+++	+++	+++	+++	++	++	+++	+++
HISAT2	+++	+++	+++	+++	+++	+++	+++	+++	++	++	++	++	+	+	+	+

*“We conclude that there is not a single mapper that is ideal in all scenarios but rather the choice of alignment tool should be driven by the application and sequencing technology.”*

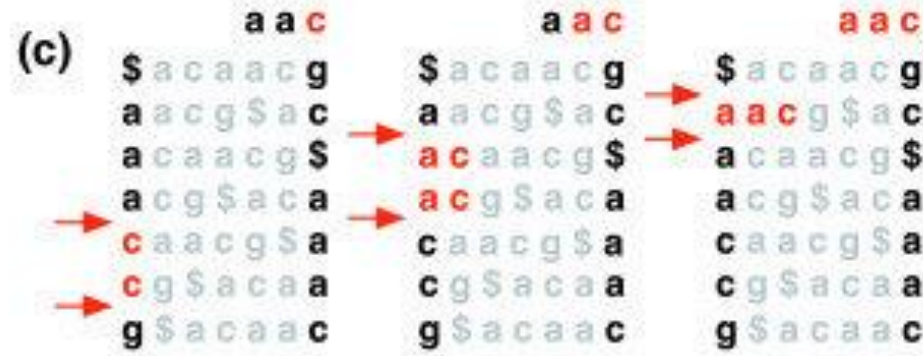
*Keel et al 2018*

# The Burrows-Wheeler Transform

Reference compression:



Searching for *aac* string:



Reconstructing original sequence:



The *i*th x in the first column corresponds to the *i*th x in the last column.



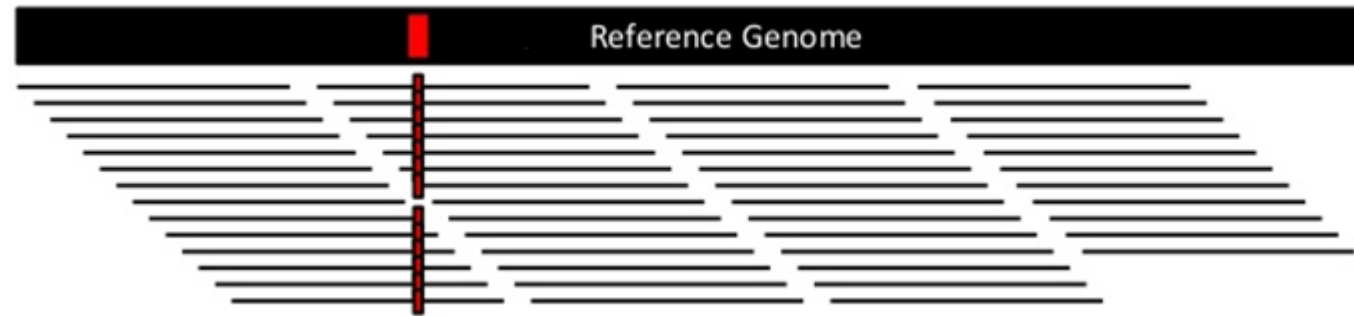
# Variant Calling

**Objective:** Identify, list and store genomic variants, either SNPs or INDELs.

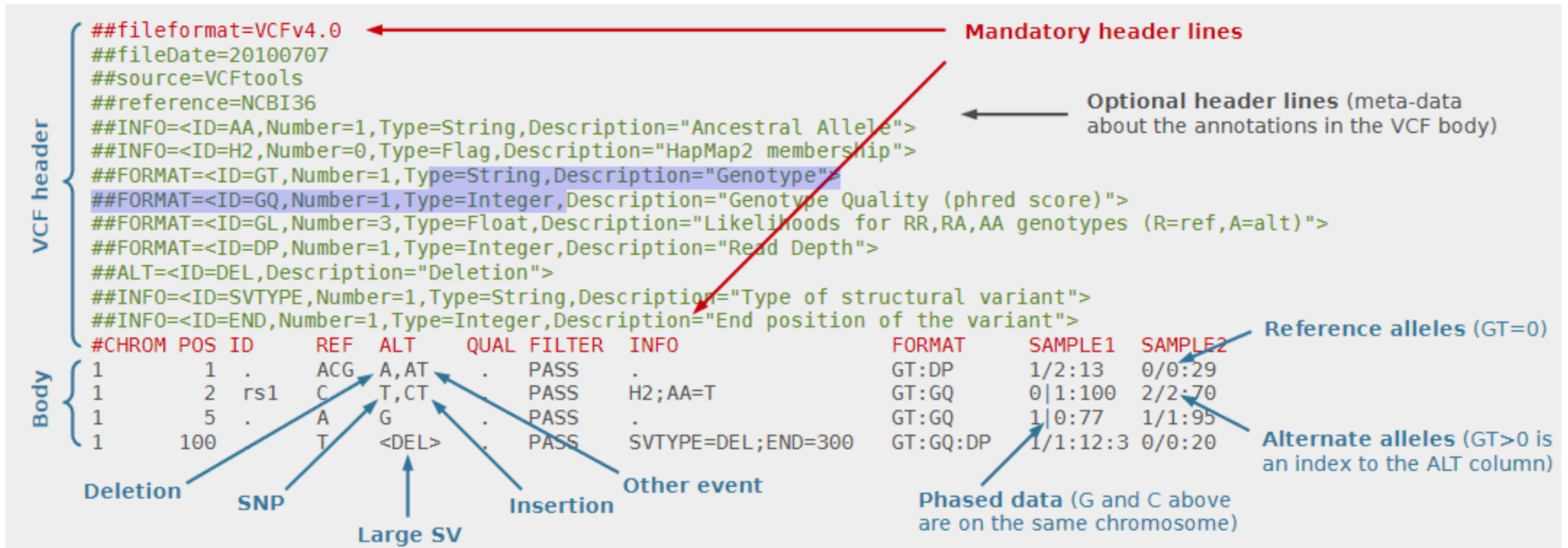
**Software:** SAMtools/BCFtools; Genome Analysis Toolkit (GATK), FreeBayes, LoFreq

**Input:** BAM/SAM files.

**Output:** VCF files



# VCF Format



<http://vcftools.sourceforge.net/VCF-poster.pdf>

See full specs:

<https://samtools.github.io/hts-specs/VCFv4.2.pdf>



# VCF Format

## Format differences between variant callers - Examples

### Finding allelic depth and filtering

#### SAMTools

NC000962\_3 69871 . C T 225 . DP=23;VDB=0.641395;SGB=-0.69168;MQSB=0.537242;MQOF=0;AC=2;AN=2;DP4=0,0,11,8;MQ=43 GT:PL  
1/1:255,57,0

```
bcftools view --include 'QUAL>=20 && INFO/DP>=10 && (INFO/DP4[2]+INFO/DP4[3])/(sum(INFO/DP4))>=0.9'
```

#### GATK

NC000962\_3 69871 . C T 810 .  
AC=1;AF=1.00;AN=1;BaseQRankSum=1.988;DP=24;Dels=0.00;FS=0.000;HaplotypeScore=0.9469;MLEAC=1;MLEAF=1.00;MQ=60.00;MQ0=0;MQRankSum=0.000  
;QD=33.75;ReadPosRankSum=1.592;SOR=0.353 GT:AD:DP:GQ:PL 1:1,23:24:99:840,0

```
bcftools view --include 'QUAL>=20 && FORMAT/DP>=10 && (FORMAT/AD[*:1])/(FORMAT/DP)>=0.9'
```

#### Freebayes

NC000962\_3 69871 . C T 656.091 .  
AB=0;ABP=0;AC=1;AF=1;AN=1;AO=23;CIGAR=1X;DP=24;DPB=24;DPRA=0;EPP=3.10471;EPPR=5.18177;GTI=0;LEN=1;MEANALT=1;MQM=60;MQMR=60;NS=1;NU  
MAL  
T=1;ODDS=151.07;PAIRED=0.956522;PAIREDR=0;PAO=0;PQA=0;PQR=0;PRO=0;QA=760;QR=14;RO=1;RPL=14;RPP=5.3706;RPPR=5.18177;RPR=9;RUN=1;SAF=12;  
SAP=3.10471;SAR=11;SRF=0;SRP=5.18177;SRR=1;TYPE=snp;technology.  
illumina=1 GT:DP:AD:RO:QR:AO:QA:GL 1:24:1,23:1:14:23:760:-67.3027,0

```
bcftools view --include 'QUAL>=20 && FORMAT/DP>=10 && (FORMAT/AO)/(FORMAT/DP)>=0.9'
```

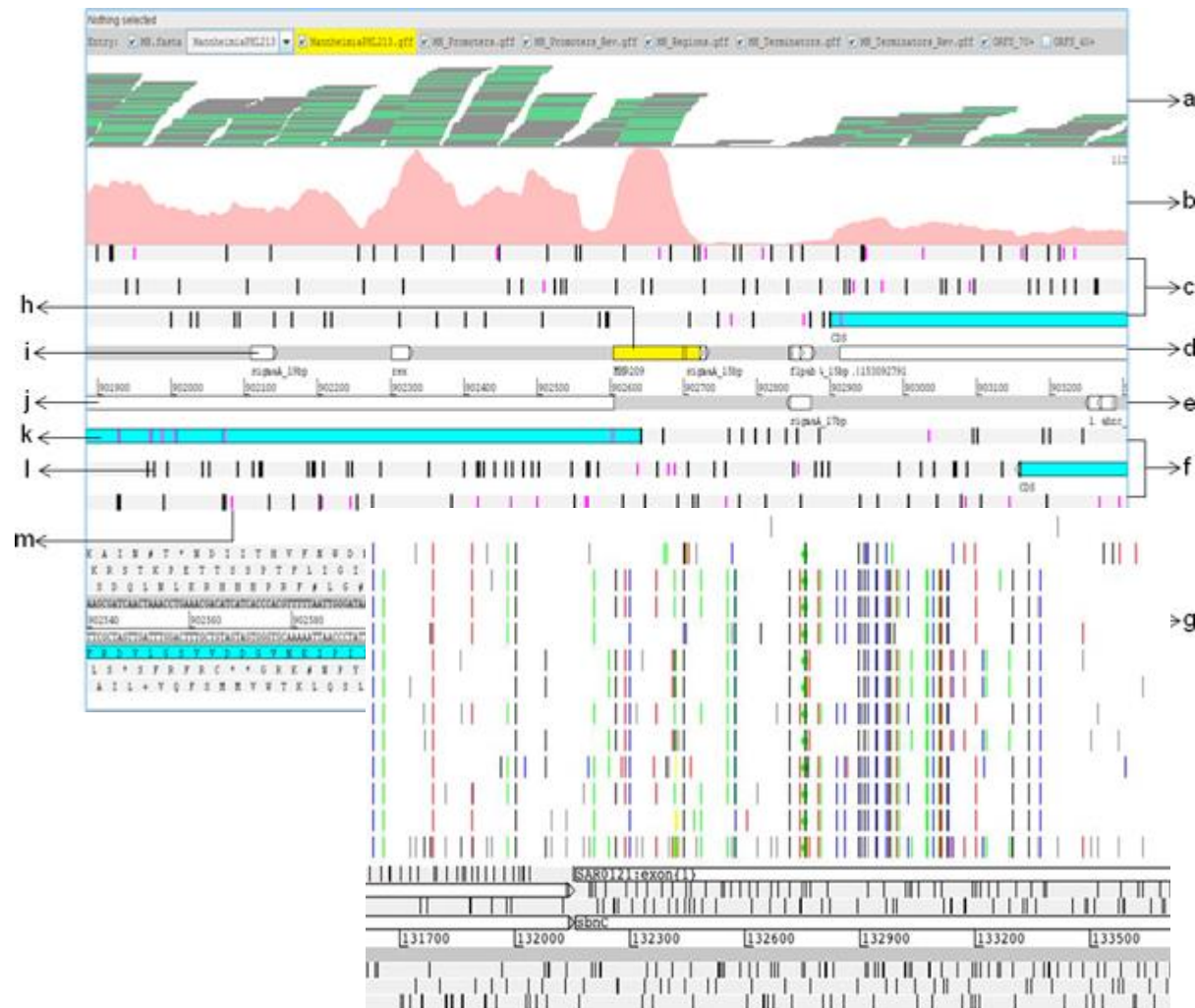
#### LoFreq

NC000962\_3 69871 . C T 732 PASS DP=24;AF=0.958333;SB=0;DP4=0,1,12,11

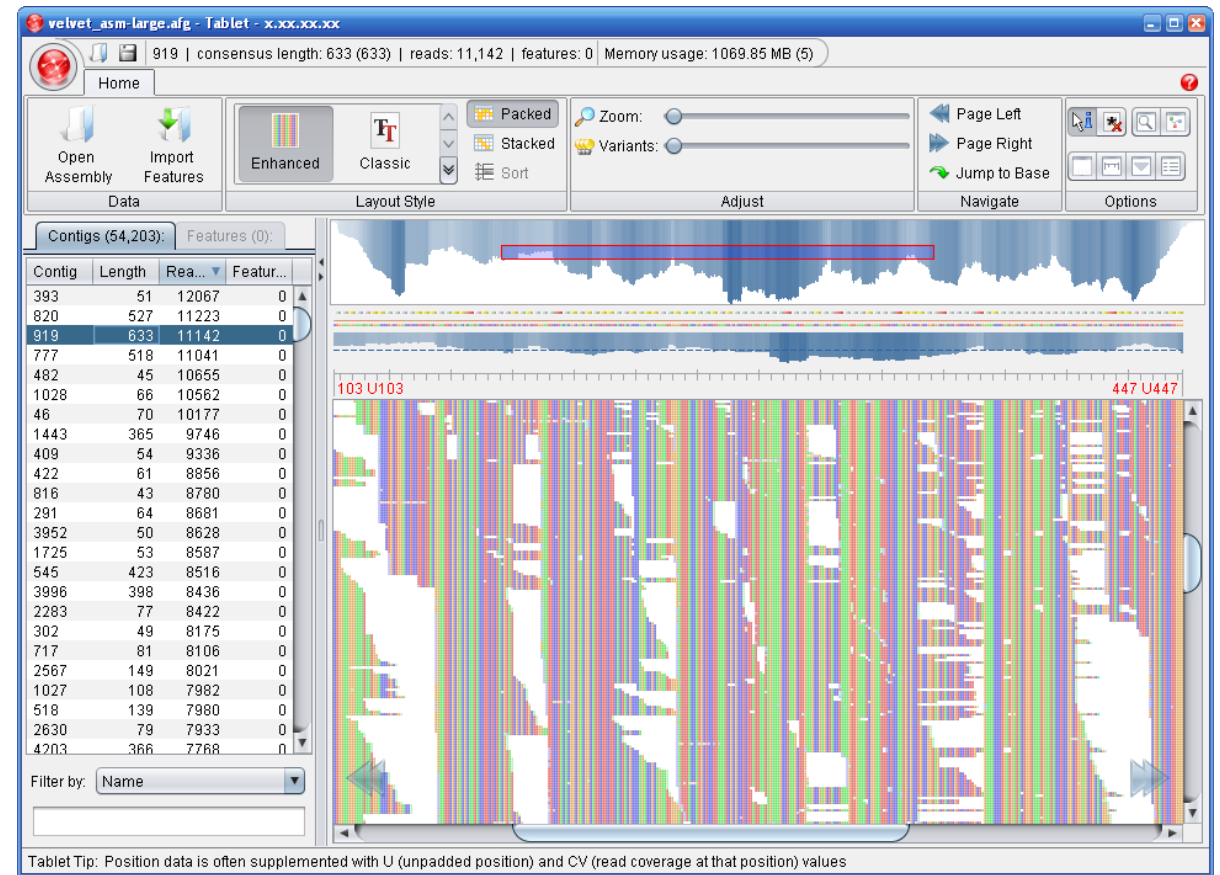
```
bcftools view --include 'QUAL>=20 && INFO/DP>=10 && (INFO/DP4[2]+INFO/DP4[3])/(sum(INFO/DP4))>=0.9'
```

# BAM and VCF Visualization

Artemis



Tablet



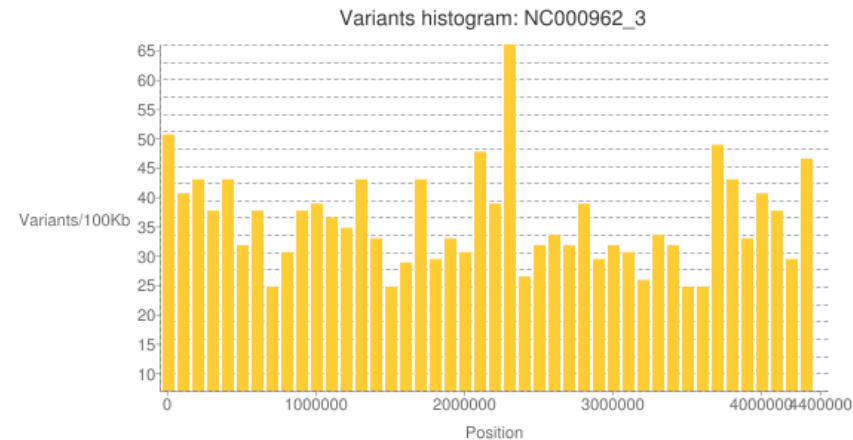
# Functional Annotation

**Objective:** Annotate each variant with its functional impact/consequence.

**Software:** SnpEff, GATK etc

**Input:** VCF files.

**Output:** Annotated VCF files



Genome	NC000962_3
Date	2021-06-17 01:39
SnpEff version	SnpEff 5.0e (build 2021-03-09 06:01), by Pablo Cingolani
Command line arguments	SnpEff -no-downstream -no-upstream NC000962_3 PT000033.filt.vcf
Warnings	124
Errors	0
Number of lines (input file)	1,597
Number of variants (before filter)	1,598
Number of not variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	1,598
Number of known variants (i.e. non-empty ID)	0 ( 0% )
Number of multi-allelic VCF entries (i.e. more than two alleles)	1
Number of effects	16,074
Genome total length	4,411,532
Genome effective length	4,411,532
Variant rate	1 variant every 2,760 bases

## Number of effects by functional class

Type (alphabetical order)	Count	Percent
MISSENSE	786	61.025%
NONSENSE	13	1.009%
SILENT	489	37.966%

Missense / Silent ratio: 1.6074

'Allele | Annotation | Annotation\_Impact | Gene\_Name | Gene\_ID | Feature\_Type | Feature\_ID | Transcript\_BioType | Rank | HGVS.c | HGVS.p | cDNA.pos / cDNA.length | CDS.pos / CDS.length | AA.pos / AA.length | Distance | ERRORS / WARNINGS / INFO' ">

ANN=G|missense\_variant|MODERATE|katG|Rv1908c|transcript|Rv1908c|protein\_coding|1/1|c.944G>C|p.Ser315Thr|944/2223|944/2223|315/740||